

R Script is a programming language widely used among statisticians, data miners, and data analysis. The software is available from [CRAN Download R](#) and [Microsoft R Open](#). Data from T3 can be accessed by

1. Saving from T3 then reading into R
2. Using BrAPI R package to read directly into R

## Download data from T3 website then read into R

1. The data can be selected by Select => Wizard or Select => Lines by Genotype Experiment

The screenshot shows the T3 website interface. The top navigation bar includes 'Select', 'Analyze', 'Download', 'Browse', 'Reports', 'Manage', and 'Resources'. The 'Select' dropdown menu is open, showing options: 'Wizard (Lines, Traits, Trials)', 'Lines by Properties', 'Lines by Phenotype', 'Lines by Haplotype', 'Lines by Genotype Experiment', 'Traits and Trials', 'Markers', 'Subset by Marker Polymorphisms', 'Genetic Map', and 'Clear selection'. The 'Lines by Genotype Experiment' option is highlighted. Below the menu, the 'Select Lines by Genotype Experiment' page is visible. It features a search bar, a 'platform' dropdown, an 'Experiments' dropdown, and a 'Lines' dropdown. A list of experiments is shown, including 'UC Davis', 'WorldwideDiversityPanel\_9K', 'USDA-ARS, North Dakota', 'NSGCwheat9K\_winter\_fac', 'NSGCwheat9K\_4X', and 'NSGCwheat9K\_spring'. A list of lines is also shown, including 'ATLAS66', 'NW03666', 'SD07220', 'LOUISE', 'CITR14695', 'PI94530', 'PI173442', 'PI119350', and 'PI48147'. A 'Save selection' button is at the bottom.

2. Go to Select => Genetic Map

**Map Sets**

This table lists the total markers in each map. If a marker is not in the the selected map set then it will be assigned to ch

select	markers (total)	markers (in selected lines)	map set name	comment (select item for complete te
<input type="radio"/>	877		Aegilops tauschii, 2009	From Luo et al, (2009) PNAS 106(37
<input type="radio"/>	19720		SynOp GBS BinMap, 2012	Bin map of Synthetic W9784 x Opata bet
<input type="radio"/>	1485		SynOp GBS AntMap, 2012	Genetic linkage map of Synthetic W9
<input type="radio"/>	1625		KleinProteo x KleinChaja, 2012	Contacts: Jorge Dubcovsky, Luxmi Tr
<input type="radio"/>	3503		wsnp 2013 Consensus	Consensus wsnp map from C.R. Cav
<input type="radio"/>	38832		90K Array Consensus	From: Wang et. al. (2014) Characteri
<input type="radio"/>	125340		CSS POPSEQ 2014	A genetic map created by locating thi
<input type="radio"/>	3393777		CSS GBS 2014	A physical map of GBS markers start a
<input checked="" type="radio"/>	168455		RefSeq v1.0	A physical map from IWGSC RefSeq
<input type="radio"/>	145004		Chromosome Survey Sequence, 2014	A physical map from the Chromosom Genome

3. Go to Download => Genotype and Phenotype Data - Select rrBLUP format
4. Select "Create File"

Download ▾
Browse ▾
Reports ▾
Manage ▾
Resources ▾

Genotype and Phenotype Data
SNP Alleles and Sequences
Marker Annotation
Bulk Download
Android Field Book
Weather Data
Genetic Maps

## Genotype and Phenotype Data

to retrieve the results.

consensus ☒ Genotype single experiment

Lines	Markers	Traits	Trials
ATLAS66 NW03666 SD07220 LOUISE CITR14695 PI94530 PI173442 PI119350 PI48147	All	none selected	none selected

Minimum MAF ≥ 5 %    Remove markers missing > 50 % of data

Removed by filtering	Remaining
73 markers have a minor allele frequency (MAF) less than 5%	
0 markers are missing more than 50% of data	
73 markers removed	6232 markers

Create file

SNP data coded as {A,C,T,G,N,+,-}  
tab delimited  
used by **TASSEL**

file type "Hapmap"  
for genetic maps the value in pos column is multiplied by 1000 and cor

Create file

genotype coded as {AA=1, BB=-1, AB=0, missing=NA}  
comma delimited  
used by **rrBLUP**

read.table("snppfile.txt", header=TRUE, check.names=FALSE)  
read.table("genotyp.hmp.txt", header=TRUE, check.names=FALSE)

Create file

genotype coded as {AA, AB, BB}  
used by **Flapjack**

Create file

**VCF** format  
used by **TASSEL**

Create file

**VCF** format  
Impute missing genotypes using Beagle

using beagle.10Jun18.811.jar (version 5.0)

5. In the R script read in file

```
R version 3.5.0 (2018-04-23) -- "Joy in Playing"  
Copyright (C) 2018 The R Foundation for Statistical Computing  
Platform: x86_64-apple-darwin15.6.0 (64-bit)
```

```
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.
```

```
Natural language support but running in an English locale
```

```
R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.
```

```
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.
```

```
> snp <- readTable("genotype.hmp.txt", header=TRUE, check.names=FALSE)
```

## **Use BrAPI R package to directly read data from T3 in R**

In R execute

```
install.packages("devtools")  
devtools::install_github("CIP-RIU/brapi")
```